

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: PlantTec Biotechnologie GmbH Forschung & Entwicklung
- (B) STREET: Hermannswerder 14
- (C) CITY: Potsdam
- (E) COUNTRY: Germany
- (F) POSTAL CODE: 14473

(ii) TITLE OF THE INVENTION: Nucleic acid molecules coding for debranching enzymes from maize

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER-READABLE VERSION:

- (A) DATA CARRIER: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Zea mays
- (F) TISSUE TYPE: Blattgewebe

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGC	ACG	AGG	TCA	AAA	CTC	CCT	CCA	GGG	TCA	GAT	TTG	CAA	CAA	GCT	GCA	48
Gly	Thr	Arg	Ser	Lys	Leu	Pro	Pro	Gly	Ser	Asp	Leu	Gln	Gln	Ala	Ala	
1				5				10						15		
ATT	GTG	GCT	ATT	CAG	GAA	GAG	GAC	CCT	TAT	AAT	TGG	GGG	TAT	AAC	CCT	96
Ile	Val	Ala	Ile	Gln	Glu	Glu	Asp	Pro	Tyr	Asn	Trp	Gly	Tyr	Asn	Pro	
			20					25					30			
GTG	GTT	TGG	GGC	GTT	CCA	AAA	GGA	AGC	TAT	GCA	AGT	AAC	CCA	GAT	GGT	144
Val	Val	Trp	Gly	Val	Pro	Lys	Gly	Ser	Tyr	Ala	Ser	Asn	Pro	Asp	Gly	
			35					40					45			

CCA	AGT	CGT	ATC	ATT	GAG	TAC	CGG	CTG	ATG	GTG	CAG	GCC	TTG	AAT	CGC	192
Pro	Ser	Arg	Ile	Ile	Glu	Tyr	Arg	Leu	Met	Val	Gln	Ala	Leu	Asn	Arg	
	50					55					60					
TTA	GGT	CTT	CGA	GTT	GTC	ATG	GAT	GTT	GTA	TAC	AAT	CAT	CTA	TAC	TCA	240
Leu	Gly	Leu	Arg	Val	Val	Met	Asp	Val	Val	Tyr	Asn	His	Leu	Tyr	Ser	
	65				70					75					80	
AGT	GGC	CCT	TTT	GCC	ATC	ACT	TCC	GTG	CTT	GAC	AAG	ATT	GTA	CCT	GGA	288
Ser	Gly	Pro	Phe	Ala	Ile	Thr	Ser	Val	Leu	Asp	Lys	Ile	Val	Pro	Gly	
				85					90					95		
TAC	TAC	CTC	AGA	AGG	GAC	TCT	AAT	GGT	CAG	ACT	GAG	AAC	AGC	GCG	GCT	336
Tyr	Tyr	Leu	Arg	Arg	Asp	Ser	Asn	Gly	Gln	Thr	Glu	Asn	Ser	Ala	Ala	
			100					105					110			
GTG	AAC	AAT	ACA	GCA	AGT	GAG	CAT	TTC	ATG	GTT	GAT	AGA	TTA	ATC	GTG	384
Val	Asn	Asn	Thr	Ala	Ser	Glu	His	Phe	Met	Val	Asp	Arg	Leu	Ile	Val	
		115					120					125				
GAT	GAC	CTT	CTG	AAT	TGG	GCA	GTA	AAT	TAC	AAA	GTT	GAC	GGG	TTC	AGA	432
Asp	Asp	Leu	Leu	Asn	Trp	Ala	Val	Asn	Tyr	Lys	Val	Asp	Gly	Phe	Arg	
	130					135					140					
TTT	GAT	CTA	ATG	GGA	CAT	ATC	ATG	AAA	AAG	ACA	ATG	ATT	AGA	GCA	AAA	480
Phe	Asp	Leu	Met	Gly	His	Ile	Met	Lys	Lys	Thr	Met	Ile	Arg	Ala	Lys	
	145				150					155					160	
TCG	GCT	CTT	CAA	AGC	CTT	ACA	ATT	GAT	GAA	CAT	GGA	GTA	GAT	GGT	TCA	528
Ser	Ala	Leu	Gln	Ser	Leu	Thr	Ile	Asp	Glu	His	Gly	Val	Asp	Gly	Ser	
				165					170					175		
AAG	ATA	TAC	TTG	TAT	GGT	GAA	GGA	TGG	AAC	TTC	GGT	GAA	GTT	GCG	GAA	576
Lys	Ile	Tyr	Leu	Tyr	Gly	Glu	Gly	Trp	Asn	Phe	Gly	Glu	Val	Ala	Glu	
			180					185					190			
AAT	CAA	CGT	GGG	ATA	AAT	GGA	TCC	CAG	CTA	AAT	ATG	AGT	GGC	ACT	GGG	624
Asn	Gln	Arg	Gly	Ile	Asn	Gly	Ser	Gln	Leu	Asn	Met	Ser	Gly	Thr	Gly	
		195					200					205				
ATT	GGT	AGT	TTC	AAC	GAT	AGA	ATC	CGT	GAT	GCT	ATA	AAT	GGT	GGC	AGT	672
Ile	Gly	Ser	Phe	Asn	Asp	Arg	Ile	Arg	Asp	Ala	Ile	Asn	Gly	Gly	Ser	
	210					215					220					
CCG	TTT	GGG	AAT	CCA	CTG	CAA	CAA	GGT	TTC	TCT	ACT	GGA	TTG	TTC	TTA	720
Pro	Phe	Gly	Asn	Pro	Leu	Gln	Gln	Gly	Phe	Ser	Thr	Gly	Leu	Phe	Leu	
	225				230					235					240	
GAG	CCA	AAT	GGA	TTT	TAT	CAG	GGC	AAT	GAA	ACA	GAG	ACA	AGG	CTC	ACG	768
Glu	Pro	Asn	Gly	Phe	Tyr	Gln	Gly	Asn	Glu	Thr	Glu	Thr	Arg	Leu	Thr	
				245				250						255		
CTT	GCT	ACA	TAC	GCT	GAC	CAT	ATA	CAG	ATT	GGA	TTA	GCT	GGC	AAT	TTG	816
Leu	Ala	Thr	Tyr	Ala	Asp	His	Ile	Gln	Ile	Gly	Leu	Ala	Gly	Asn	Leu	
			260					265					270			
AAG	GAC	TAT	GTA	GTT	ATA	TCT	CAT	ACT	GGA	GAA	GCT	AGA	AAA	GGA	TCT	864
Lys	Asp	Tyr	Val	Val	Ile	Ser	His	Thr	Gly	Glu	Ala	Arg	Lys	Gly	Ser	
		275					280					285				

GAA ATT CGC ACC TTC GAT GGC TCA CCA GTT GGC TAT GCT TCA TCC CCT	912
Glu Ile Arg Thr Phe Asp Gly Ser Pro Val Gly Tyr Ala Ser Ser Pro	
290 295 300	
ATA GAA ACA ATA AAC TAC GCC TCT GCT CAT GAC AAT GAA ACA CTA TTT	960
Ile Glu Thr Ile Asn Tyr Ala Ser Ala His Asp Asn Glu Thr Leu Phe	
305 310 315 320	
GAT ATT ATT AGT CTA AAG ACT CCG ATG GAC CTC TCA ATT GAC GAG CGA	1008
Asp Ile Ile Ser Leu Lys Thr Pro Met Asp Leu Ser Ile Asp Glu Arg	
325 330 335	
TGC AGG ATA AAT CAT TTG TCC ACA AGC ATG ATT GCA TTA TCC CAG CGA	1056
Cys Arg Ile Asn His Leu Ser Thr Ser Met Ile Ala Leu Ser Gln Gly	
340 345 350	
ATA CCA TTT TTT CAT GCT GGT GAT GAG ATA CTA CGA TCT AAG TCG CTT	1104
Ile Pro Phe Phe His Ala Gly Asp Glu Ile Leu Arg Ser Lys Ser Leu	
355 360 365	
GAT CGA GAT TCA TAT GAC TCT GGT GAT TGG TTT AAC AAG ATT GAT TTT	1152
Asp Arg Asp Ser Tyr Asp Ser Gly Asp Trp Phe Asn Lys Ile Asp Phe	
370 375 380	
ACC TAT GAA ACA AAC AAT TGG GGT GTT GGG CTT CCA CCA AGA GAA AAG	1200
Thr Tyr Glu Thr Asn Asn Trp Gly Val Gly Leu Pro Pro Arg Glu Lys	
385 390 395 400	
AAC GAA GGG AGC TGG CCT TTG ATG AAG CCA AGA TTG GAG AAC CCG TCG	1248
Asn Glu Gly Ser Trp Pro Leu Met Lys Pro Arg Leu Glu Asn Pro Ser	
405 410 415	
TTC AAA CCT GCA AAA CAT GAC ATT ATT GCT GCC TTA GAC AAA TTT ATT	1296
Phe Lys Pro Ala Lys His Asp Ile Ile Ala Ala Leu Asp Lys Phe Ile	
420 425 430	
GAT ATC CTC AAG ATC AGA TAC TCA TCA CCT CTC TTT CGC CTA ACT ACA	1344
Asp Ile Leu Lys Ile Arg Tyr Ser Ser Pro Leu Phe Arg Leu Thr Thr	
435 440 445	
GCA AGT GAT ATT GTG CAA AGG GTT CAC TTT CAC AAC ACA GGG CCC TCC	1392
Ala Ser Asp Ile Val Gln Arg Val His Phe His Asn Thr Gly Pro Ser	
450 455 460	
TTG GTT CCA GGA GTT ATT GTC ATG AGC ATC GAA GAT GCA CGA AAT GAT	1440
Leu Val Pro Gly Val Ile Val Met Ser Ile Glu Asp Ala Arg Asn Asp	
465 470 475 480	
AGG CAT GAT ATG GCC CAG ATA GAT GAA ACA TTC TCT TGT GTC GTT ACA	1488
Arg His Asp Met Ala Gln Ile Asp Glu Thr Phe Ser Cys Val Val Thr	
485 490 495	
GTC TTC AAT GTA TGT CCG TAC GAA GTG TCT ATA GAA ATC CCT GAT CTT	1536
Val Phe Asn Val Cys Pro Tyr Glu Val Ser Ile Glu Ile Pro Asp Leu	
500 505 510	
GCA TCA CTG CGG CTT CAG TTG CAT CCA GTG CAG GTG AAT TCA TCG GAT	1584
Ala Ser Leu Arg Leu Gln Leu His Pro Val Gln Val Asn Ser Ser Asp	
515 520 525	

GCG TTA GCC AGG CAG TCT GCG TAC GAC ACC GCC ACA GGT CGA TTC ACC	1632
Ala Leu Ala Arg Gln Ser Ala Tyr Asp Thr Ala Thr Gly Arg Phe Thr	
530 535 540	
GTG CCG AAA AGG ACA GCA GCA GTG TTC GTG GAA CCC AGG TGC T	1675
Val Pro Lys Arg Thr Ala Ala Val Phe Val Glu Pro Arg Cys	
545 550 555	
GATGGATGCC TTTCGCTAGC GAGCAAGTGC ATTCGGCATC CAAGTCGAAG CAAACGAATG	1735
AAATAAGAGA AGGCCATCGA ATAAAACGAA GTATATAAAT AGATTGAATA AGACGTTGCC	1795
CAAGTTGCCA AGGCACGCTT TGCCATATGT ATGCGTTGAA AAATAAATAA ATAAATAAAT	1855
AAATGATGTT ATAGAGGTAC AAAAGCATTG GAACATTTCT TTATAGAGGT GAACCACCCT	1915
ATTTTCCAGT TTCCATGTGT GAATTGTGAT TAGCATATGT ATGGAATAAT AATATAAATT	1975
AATTTTATGC AAAAAAAA	1993

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Gly Thr Arg Ser Lys Leu Pro Pro Gly Ser Asp Leu Gln Gln Ala Ala	
1 5 10 15	
Ile Val Ala Ile Gln Glu Glu Asp Pro Tyr Asn Trp Gly Tyr Asn Pro	
20 25 30	
Val Val Trp Gly Val Pro Lys Gly Ser Tyr Ala Ser Asn Pro Asp Gly	
35 40 45	
Pro Ser Arg Ile Ile Glu Tyr Arg Leu Met Val Gln Ala Leu Asn Arg	
50 55 60	
Leu Gly Leu Arg Val Val Met Asp Val Val Tyr Asn His Leu Tyr Ser	
65 70 75 80	
Ser Gly Pro Phe Ala Ile Thr Ser Val Leu Asp Lys Ile Val Pro Gly	
85 90 95	
Tyr Tyr Leu Arg Arg Asp Ser Asn Gly Gln Thr Glu Asn Ser Ala Ala	
100 105 110	
Val Asn Asn Thr Ala Ser Glu His Phe Met Val Asp Arg Leu Ile Val	
115 120 125	
Asp Asp Leu Leu Asn Trp Ala Val Asn Tyr Lys Val Asp Gly Phe Arg	
130 135 140	

Phe Asp Leu Met Gly His Ile Met Lys Lys Thr Met Ile Arg Ala Lys
 145 150 155 160
 Ser Ala Leu Gln Ser Leu Thr Ile Asp Glu His Gly Val Asp Gly Ser
 165 170 175
 Lys Ile Tyr Leu Tyr Gly Glu Gly Trp Asn Phe Gly Glu Val Ala Clu
 180 185 190
 Asn Gln Arg Gly Ile Asn Gly Ser Gln Leu Asn Met Ser Gly Thr Gly
 195 200 205
 Ile Gly Ser Phe Asn Asp Arg Ile Arg Asp Ala Ile Asn Gly Gly Ser
 210 215 220
 Pro Phe Gly Asn Pro Leu Gln Gln Gly Phe Ser Thr Gly Leu Phe Leu
 225 230 235 240
 Glu Pro Asn Gly Phe Tyr Gln Gly Asn Glu Thr Glu Thr Arg Leu Thr
 245 250 255
 Leu Ala Thr Tyr Ala Asp His Ile Gln Ile Gly Leu Ala Gly Asn Leu
 260 265 270
 Lys Asp Tyr Val Val Ile Ser His Thr Gly Glu Ala Arg Lys Gly Ser
 275 280 285
 Glu Ile Arg Thr Phe Asp Gly Ser Pro Val Gly Tyr Ala Ser Ser Pro
 290 295 300
 Ile Glu Thr Ile Asn Tyr Ala Ser Ala His Asp Asn Glu Thr Leu Phe
 305 310 315 320
 Asp Ile Ile Ser Leu Lys Thr Pro Met Asp Leu Ser Ile Asp Glu Arg
 325 330 335
 Cys Arg Ile Asn His Leu Ser Thr Ser Met Ile Ala Leu Ser Gln Gly
 340 345 350
 Ile Pro Phe Phe His Ala Gly Asp Glu Ile Leu Arg Ser Lys Ser Leu
 355 360 365
 Asp Arg Asp Ser Tyr Asp Ser Gly Asp Trp Phe Asn Lys Ile Asp Phe
 370 375 380
 Thr Tyr Glu Thr Asn Asn Trp Gly Val Gly Leu Pro Pro Arg Glu Lys
 385 390 395 400
 Asn Glu Gly Ser Trp Pro Leu Met Lys Pro Arg Leu Glu Asn Pro Ser
 405 410 415
 Phe Lys Pro Ala Lys His Asp Ile Ile Ala Ala Leu Asp Lys Phe Ile
 420 425 430
 Asp Ile Leu Lys Ile Arg Tyr Ser Ser Pro Leu Phe Arg Leu Thr Thr
 435 440 445
 Ala Ser Asp Ile Val Gln Arg Val His Phe His Asn Thr Cly Pro Ser
 450 455 460

Leu Val Pro Gly Val Ile Val Met Ser Ile Glu Asp Ala Arg Asn Asp 480
 465 470 475
 Arg His Asp Met Ala Gln Ile Asp Glu Thr Phe Ser Cys Val Val Thr 495
 485 490
 Val Phe Asn Val Cys Pro Tyr Glu Val Ser Ile Glu Ile Pro Asp Leu 510
 500 505
 Ala Ser Leu Arg Leu Gln Leu His Pro Val Gln Val Asn Ser Ser Asp 525
 515 520
 Ala Leu Ala Arg Gln Ser Ala Tyr Asp Thr Ala Thr Gly Arg Phe Thr 540
 530 535
 Val Pro Lys Arg Thr Ala Ala Val Phe Val Glu Pro Arg Cys 555
 545 550

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE DESCRIPTION:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Solanum tuberosum
- (B) STRAIN: Berolina
- (F) TISSUE TYPE: tuber

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LAGE:1..492
- (D) OTHER INFORMATION:/product= "debranching enzyme (R-enzyme) "

(xi) SEQUENCE INFORMATION: SEQ ID NO: 3:

TCT GCT GAT GGC AAG TGG ACA TTA TTA GTT AAT CTT GAT TCT GAT GAT	48
Ser Ala Asp Gly Lys Trp Thr Leu Leu Val Asn Leu Asp Ser Asp Asp	
560 565 570	
GTA AAA CCT GAA GGC TGG GAT AAT CTA CAA GAC GTG AAG CCA AAT CTT	96
Val Lys Pro Glu Gly Trp Asp Asn Leu Gln Asp Val Lys Pro Asn Leu	
575 580 585 590	
CTT TCC TTT TCT GAT GTC AGC ATC TAT GAG CTG CAT GTT AGA GAT TTC	144
Leu Ser Phe Ser Asp Val Ser Ile Tyr Glu Leu His Val Arg Asp Phe	
595 600 605	

ACT GCC AGT GAC CCT ACT GTG TCT CAT GAA TTT CAG GCC GGT TAT CTC	192
Thr Ala Ser Asp Pro Thr Val Ser His Glu Phe Gln Ala Gly Tyr Leu	
610 615 620	
GCC CCT TCC ACG TCG CAG GCA TCA GCT GGT GTC CAA CAT TTG AAA AGA	240
Ala Pro Ser Thr Ser Gln Ala Ser Ala Gly Val Gln His Leu Lys Arg	
625 630 635	
TTA TCA AGT GCT GGT ATC ACT CAT GTC CAC CTG TGG CCA ACC TAT CAA	288
Leu Ser Ser Ala Gly Ile Thr His Val His Leu Trp Pro Thr Tyr Gln	
640 645 650	
TTT GCT GGT GTC GAA GAT GAG AAA CAT AAA TGG AAG TAT ACA GAT ATC	336
Phe Ala Gly Val Glu Asp Glu Lys His Lys Trp Lys Tyr Thr Asp Ile	
655 660 665 670	
GAG AAA CTC AAC TCT TTT CCA CCA GAT TCT GAG GAG CAG CAG GCT CTT	384
Glu Lys Leu Asn Ser Phe Pro Pro Asp Ser Glu Glu Gln Gln Ala Leu	
675 680 685	
ATC ACA GCC ATC CAA GAT GAA GAT GGC TAT AAT TGG GGG TAT AAT CCT	432
Ile Thr Ala Ile Gln Asp Glu Asp Gly Tyr Asn Trp Gly Tyr Asn Pro	
690 695 700	
GTT CTC TGG GGA GTT CCA AAG GGA AGC TAT GCT GGT AAT GCA AAT GGT	480
Val Leu Trp Gly Val Pro Lys Gly Ser Tyr Ala Gly Asn Ala Asn Gly	
705 710 715	
CCT TGT CGT ATC	492
Pro Cys Arg Ile	
720	

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Ser Ala Asp Gly Lys Trp Thr Leu Leu Val Asn Leu Asp Ser Asp Asp	
1 5 10 15	
Val Lys Pro Glu Gly Trp Asp Asn Leu Gln Asp Val Lys Pro Asn Leu	
20 25 30	
Leu Ser Phe Ser Asp Val Ser Ile Tyr Glu Leu His Val Arg Asp Phe	
35 40 45	
Thr Ala Ser Asp Pro Thr Val Ser His Glu Phe Gln Ala Gly Tyr Leu	
50 55 60	
Ala Pro Ser Thr Ser Gln Ala Ser Ala Gly Val Gln His Leu Lys Arg	
65 70 75 80	

Leu Ser Ser Ala Gly Ile Thr His Val His Leu Trp Pro Thr Tyr Gln
 85 90 95
 Phe Ala Gly Val Glu Asp Glu Lys His Lys Trp Lys Tyr Thr Asp Ile
 100 105 110
 Glu Lys Leu Asn Ser Phe Pro Pro Asp Ser Glu Glu Gln Gln Ala Leu
 115 120 125
 Ile Thr Ala Ile Gln Asp Glu Asp Gly Tyr Asn Trp Gly Tyr Asn Pro
 130 135 140
 Val Leu Trp Gly Val Pro Lys Gly Ser Tyr Ala Gly Asn Ala Asn Gly
 145 150 155 160
 Pro Cys Arg Ile

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